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## RAW SEQUENCE LISTING

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Application Serial Number: 10/528,992  
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## RAW SEQUENCE LISTING

DATE: 03/31/2006

PATENT APPLICATION: US/10/528,992

TIME: 11:06:40

Input Set : A:\2006-01-06 0020-5361PUS1.ST25.txt

Output Set: N:\CRF4\03292006\J528992.raw

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3 <110> APPLICANT: Nobuyuki YOSHIDA
4     Yoshiki TANI
5     Satoshi YONEHARA
7 <120> TITLE OF INVENTION: FRUCTOSYLAMINE OXIDASE
9 <130> FILE REFERENCE: 0020-5361PUS1
11 <140> CURRENT APPLICATION NUMBER: US 10/528,992
12 <141> CURRENT FILING DATE: 2005-03-24
14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/11766
15 <151> PRIOR FILING DATE: 2003-09-16
17 <150> PRIOR APPLICATION NUMBER: JP 2002-277214
18 <151> PRIOR FILING DATE: 2002-09-24
20 <150> PRIOR APPLICATION NUMBER: JP 2002-309734
21 <151> PRIOR FILING DATE: 2002-10-24
23 <160> NUMBER OF SEQ ID NOS: 8
25 <170> SOFTWARE: PatentIn version 3.1
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28 <211> LENGTH: 460
29 <212> TYPE: DNA
30 <213> ORGANISM: Fusarium proliferatum
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37 aaaccataaa taaatcaaaa ctttcaacaa cggatctctt gggtctggca tcgatgaaga      180
39 acgcagcaaa atgcgataag taatgtgaat tgcagaattc agtgaatcat cgaatctttg      240
41 aacgcacatt gcgcccgcga gtattctggc gggcatgcct gttcgagcgt catttcaacc      300
43 ctcaagcccc cgggtttggt gttggggatc ggcgagccct tgcggcaagc cggccccgaa      360
45 atctagtggc ggtctcgctg cagcttccat tgcgtagtag taaaaccctc gcaactggta      420
47 cgcggcgcgg ccaagccgtt aaaccccaa cttctgaatg      460
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51 <211> LENGTH: 10
52 <212> TYPE: PRT
53 <213> ORGANISM: Fusarium proliferatum
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61 <211> LENGTH: 1422
62 <212> TYPE: DNA
63 <213> ORGANISM: Fusarium proliferatum
65 <220> FEATURE:
66 <221> NAME/KEY: CDS
67 <222> LOCATION: (1)..(1419)
69 <400> SEQUENCE: 3

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71 Met Ala Gly Pro Pro Ser Ser Ile Leu Ile Val Gly Ser Gly Val Phe
72 1          5          10          15
74 ggg ctc ggt acc gcc tgg gct ttg gcc aaa cga tca cac ttt tcc aac      96
75 Gly Leu Gly Thr Ala Trp Ala Leu Ala Lys Arg Ser His Phe Ser Asn
76          20          25          30
78 acc tcg att act gtc gtc gac gac tgc gca gga cag ttt cct cca gaa      144
79 Thr Ser Ile Thr Val Val Asp Asp Cys Ala Gly Gln Phe Pro Pro Glu
80          35          40          45
82 gat gct gcc agt gta gac tcg tct cgc att gta cga gcc gac tac tcg      192
83 Asp Ala Ala Ser Val Asp Ser Ser Arg Ile Val Arg Ala Asp Tyr Ser
84          50          55          60
86 gac cct tac tat gcc gcg ctt gcc gcc gag gcg cag aag gaa tgg cga      240
87 Asp Pro Tyr Tyr Ala Ala Leu Ala Ala Glu Ala Gln Lys Glu Trp Arg
88 65          70          75          80
90 aag cag ggt gat cat gag gtc ggt ggg cag gga cga tat tcc gag tcg      288
91 Lys Gln Gly Asp His Glu Val Gly Gly Gln Gly Arg Tyr Ser Glu Ser
92          85          90          95
94 ggc ttt gtt ctc tgc gcg agc gag act cct gaa gac ttc aag ctc aag      336
95 Gly Phe Val Leu Cys Ala Ser Glu Thr Pro Glu Asp Phe Lys Leu Lys
96          100          105          110
98 aag tct ggc atg gac tac acc aag gag agc gcc aaa aac gtc gag ttg      384
99 Lys Ser Gly Met Asp Tyr Thr Lys Glu Ser Ala Lys Asn Val Glu Leu
100          115          120          125
102 att gct aag gag act ggt ctg ccc gtg gat aag atc cag aag ctg gag      432
103 Ile Ala Lys Glu Thr Gly Leu Pro Val Asp Lys Ile Gln Lys Leu Glu
104          130          135          140
106 agt acc aag gct ctc caa gag ttc ctt ggc aca gac ggt tat ccc gga      480
107 Ser Thr Lys Ala Leu Gln Glu Phe Leu Gly Thr Asp Gly Tyr Pro Gly
108 145          150          155          160
110 gac tgg ggc tac ctc aat ggc aac tct ggc tgg gct gat gcc ggg gag      528
111 Asp Trp Gly Tyr Leu Asn Gly Asn Ser Gly Trp Ala Asp Ala Gly Glu
112          165          170          175
114 ggt atg aag tgg ctc tat aag cag gcc cag gcc aca gga cgt att cat      576
115 Gly Met Lys Trp Leu Tyr Lys Gln Ala Gln Ala Thr Gly Arg Ile His
116          180          185          190
118 ttt gtc aac ggc aag gtg aca gag ctc gta aca gag ggt gac cga gtc      624
119 Phe Val Asn Gly Lys Val Thr Glu Leu Val Thr Glu Gly Asp Arg Val
120          195          200          205
122 att ggt gcg aaa ttg agc gat tca aag att ctc aag gcc gat gtg gtt      672
123 Ile Gly Ala Lys Leu Ser Asp Ser Lys Ile Leu Lys Ala Asp Val Val
124          210          215          220
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128 225          230          235          240
130 aga aca gag gct act ggc cat gct gtc gcg tat atg gac atc aca ccg      768
131 Arg Thr Glu Ala Thr Gly His Ala Val Ala Tyr Met Asp Ile Thr Pro
132          245          250          255
134 gaa gag cag aag cga ctc gac aac ttc cct gtg gtg ttg aat ctc agc      816

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135 Glu Glu Gln Lys Arg Leu Asp Asn Phe Pro Val Val Leu Asn Leu Ser
136          260          265          270
138 acc ggt ctc ttc ctc att cct cct cga aat aac gtc ctc aag gcc gcc      864
139 Thr Gly Leu Phe Leu Ile Pro Pro Arg Asn Asn Val Leu Lys Ala Ala
140          275          280          285
142 cga cac aca ttc ggg tac att aac ccg gtc aag att aac aac gct ctt      912
143 Arg His Thr Phe Gly Tyr Ile Asn Pro Val Lys Ile Asn Asn Ala Leu
144          290          295          300
146 cct cct tcg ccc aac gat aag cgg gaa cca ttc atc gca tct caa ccc      960
147 Pro Pro Ser Pro Asn Asp Lys Arg Glu Pro Phe Ile Ala Ser Gln Pro
148 305          310          315          320
150 tac acc tct cgc aac gat tcc tca aat cct tta acc gtc gag gct gac      1008
151 Tyr Thr Ser Arg Asn Asp Ser Ser Asn Pro Leu Thr Val Glu Ala Asp
152          325          330          335
154 aaa gat ctg cgc cgc gca ctc acg gat ctg tgt cct ata cgt ggc cta      1056
155 Lys Asp Leu Arg Arg Ala Leu Thr Asp Leu Cys Pro Ile Arg Gly Leu
156          340          345          350
158 gaa acc agg cca tgg aag gag gct cga atc tgc tgg tat tcc gat aca      1104
159 Glu Thr Arg Pro Trp Lys Glu Ala Arg Ile Cys Trp Tyr Ser Asp Thr
160          355          360          365
162 cga gat ggc gag tgg ctc att gac tac cac ccg ggc tgg aag gga ctc      1152
163 Arg Asp Gly Glu Trp Leu Ile Asp Tyr His Pro Gly Trp Lys Gly Leu
164          370          375          380
166 ttt gtt gca aca ggt gac agt gga cac gga ttc aag ttc cta ccc aac      1200
167 Phe Val Ala Thr Gly Asp Ser Gly His Gly Phe Lys Phe Leu Pro Asn
168 385          390          395          400
170 ttg ggt gag aaa atc gtg gat gtt atg caa ggc cag ggt ggc aag ctt      1248
171 Leu Gly Glu Lys Ile Val Asp Val Met Gln Gly Gln Gly Gly Lys Leu
172          405          410          415
174 ggc gag aag tgg cga tgg aaa gag atc cag aat gat gga gtc gga aga      1296
175 Gly Glu Lys Trp Arg Trp Lys Glu Ile Gln Asn Asp Gly Val Gly Arg
176          420          425          430
178 gag acg aac gga gtg tac act ggt tta gtg acg gaa gat ggt agc aga      1344
179 Glu Thr Asn Gly Val Tyr Thr Gly Leu Val Thr Glu Asp Gly Ser Arg
180          435          440          445
182 ggt gga cgg ccc ttg gtg ctc tgt gat gag ctc gag aag ggc agg gcg      1392
183 Gly Gly Arg Pro Leu Val Leu Cys Asp Glu Leu Glu Lys Gly Arg Ala
184          450          455          460
186 ctt att ggg aac acc aag gcc aag cta tga      1422
187 Leu Ile Gly Asn Thr Lys Ala Lys Leu
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192 <211> LENGTH: 473
193 <212> TYPE: PRT
194 <213> ORGANISM: Fusarium proliferatum
196 <400> SEQUENCE: 4
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202			20				25			30			
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206			35				40			45			
208	Asp	Ala	Ala	Ser	Val	Asp	Ser	Ser	Arg	Ile	Val	Arg	Ala
209		50					55				60		
211	Asp	Pro	Tyr	Tyr	Ala	Ala	Leu	Ala	Ala	Glu	Ala	Gln	Lys
212	65					70				75			80
214	Lys	Gln	Gly	Asp	His	Glu	Val	Gly	Gly	Gln	Gly	Arg	Tyr
215				85					90				95
217	Gly	Phe	Val	Leu	Cys	Ala	Ser	Glu		Glu	Asp	Phe	Lys
218				100									110
220	Lys	Ser	Gly	Met	Asp	Tyr	Thr	Lys	Glu	Ser	Ala	Lys	Asn
221			115					120					125
223	Ile	Ala	Lys	Glu	Thr	Gly	Leu	Pro	Val	Asp	Lys	Ile	Gln
224		130					135					140	
226	Ser	Thr	Lys	Ala	Leu	Gln	Glu	Phe	Leu	Gly	Thr	Asp	Gly
227	145					150					155		160
229	Asp	Trp	Gly	Tyr	Leu	Asn	Gly	Asn	Ser	Gly	Trp	Ala	Asp
230				165						170			175
232	Gly	Met	Lys	Trp	Leu	Tyr	Lys	Gln	Ala	Gln	Ala	Thr	Gly
233				180				185					190
235	Phe	Val	Asn	Gly	Lys	Val	Thr	Glu	Leu	Val	Thr	Glu	Gly
236		195						200				205	
238	Ile	Gly	Ala	Lys	Leu	Ser	Asp	Ser	Lys	Ile	Leu	Lys	Ala
239		210					215				220		
241	Met	Val	Ala	Ala	Gly	Ala	Trp	Ser	Gly	Ser	Leu	Val	Asp
242	225				230						235		240
244	Arg	Thr	Glu	Ala	Thr	Gly	His	Ala	Val	Ala	Tyr	Met	Asp
245				245						250			255
247	Glu	Glu	Gln	Lys	Arg	Leu	Asp	Asn	Phe	Pro	Val	Val	Leu
248			260					265					270
250	Thr	Gly	Leu	Phe	Leu	Ile	Pro	Pro	Arg	Asn	Asn	Val	Leu
251			275					280				285	
253	Arg	His	Thr	Phe	Gly	Tyr	Ile	Asn	Pro	Val	Lys	Ile	Asn
254		290				295					300		
256	Pro	Pro	Ser	Pro	Asn	Asp	Lys	Arg	Glu	Pro	Phe	Ile	Ala
257	305				310						315		320
259	Tyr	Thr	Ser	Arg	Asn	Asp	Ser	Ser	Asn	Pro	Leu	Thr	Val
260				325						330			335
262	Lys	Asp	Leu	Arg	Arg	Ala	Leu	Thr	Asp	Leu	Cys	Pro	Ile
263			340					345					350
265	Glu	Thr	Arg	Pro	Trp	Lys	Glu	Ala	Arg	Ile	Cys	Trp	Tyr
266		355					360					365	
268	Arg	Asp	Gly	Glu	Trp	Leu	Ile	Asp	Tyr	His	Pro	Gly	Trp
269		370				375					380		
271	Phe	Val	Ala	Thr	Gly	Asp	Ser	Gly	His	Gly	Phe	Lys	Phe
272	385				390					395			400
274	Leu	Gly	Glu	Lys	Ile	Val	Asp	Val	Met	Gln	Gly	Gln	Gly
275				405					410				415

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277 Gly Glu Lys Trp Arg Trp Lys Glu Ile Gln Asn Asp Gly Val Gly Arg
278          420          425          430
280 Glu Thr Asn Gly Val Tyr Thr Gly Leu Val Thr Glu Asp Gly Ser Arg
281          435          440          445
283 Gly Gly Arg Pro Leu Val Leu Cys Asp Glu Leu Glu Lys Gly Arg Ala
284          450          455          460
286 Leu Ile Gly Asn Thr Lys Ala Lys Leu
287 465          470
290 <210> SEQ ID NO: 5
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292 <212> TYPE: DNA
293 <213> ORGANISM: Fusarium proliferatum
295 <220> FEATURE:
296 <221> NAME/KEY: CDS
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303 1          5          10          15
305 gtt ggt ggc gga act tgg gga tgc tca act gcc ctc cat ctc gcc cgt      96
306 Val Gly Gly Gly Thr Trp Gly Cys Ser Thr Ala Leu His Leu Ala Arg
307          20          25          30
309 cgg ggt tac acc aac gtc act gtt ctc gat gtc aat cgc atc ccg tca      144
310 Arg Gly Tyr Thr Asn Val Thr Val Leu Asp Val Asn Arg Ile Pro Ser
311          35          40          45
313 ccg ata tca gcc ggg cat gat gta aac aaa ctt tct aac aga cta ggc      192
314 Pro Ile Ser Ala Gly His Asp Val Asn Lys Leu Ser Asn Arg Leu Gly
315          50          55          60
317 act tct gat agt aaa ggc gat gac gaa gac tca atc tgg aaa gct ctt      240
318 Thr Ser Asp Ser Lys Gly Asp Asp Glu Asp Ser Ile Trp Lys Ala Leu
319 65          70          75          80
321 acg tac gcc gca gct caa gga tgg ctc cat gat ccc atc ttc caa cct      288
322 Thr Tyr Ala Ala Ala Gln Gly Trp Leu His Asp Pro Ile Phe Gln Pro
323          85          90          95
325 ttc tgc cac aat aca gga gct gtc atg gct ggc tca aca cca aaa tct      336
326 Phe Cys His Asn Thr Gly Ala Val Met Ala Gly Ser Thr Pro Lys Ser
327          100          105          110
329 atc aag cag ctg gta gaa gat gag atc ggt gac gac atc gac cag tat      384
330 Ile Lys Gln Leu Val Glu Asp Glu Ile Gly Asp Asp Ile Asp Gln Tyr
331          115          120          125
333 aca cct ctc aac aca gca gaa gat ttc aga agg act atg ccg gag cgt      432
334 Thr Pro Leu Asn Thr Ala Glu Asp Phe Arg Arg Thr Met Pro Glu Arg
335          130          135          140
337 att ctg aca ggt gat ttt cta ggc tgg aag ggc ttt tac aag ccc aga      480
338 Ile Leu Thr Gly Asp Phe Leu Gly Trp Lys Gly Phe Tyr Lys Pro Arg
339 145          150          155          160
341 ggt tca ggt tgg gtt cat gcc aga aag gct atg aaa gct gct ttt gaa      528
342 Gly Ser Gly Trp Val His Ala Arg Lys Ala Met Lys Ala Ala Phe Glu
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**VERIFICATION SUMMARY**

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